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SEQ ID NO: 6 A33 1 M V G K M W P V L W T L C A V R V T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S  
SEQ ID NO: 1 40628 1 M G T K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E . . . . . P E V R I P E  
SEQ ID NO: 2 45416 1 . . . . M G I L L G L L L L G H L T V D T Y G R P I L E V P E S V T G P W K G O V N L P C T Y D P L  
SEQ ID NO: 9 35638 1 M A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q . . . . . Q V V T A V E  
SEQ ID NO: 10 JAM 1 . M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q . . . . . S D V Q V P E

A33 51 S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D A  
40628 43 N N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D R V T F L P T  
45416 47 Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D V  
35638 43 Y Q E A I L A C K T P K X T V S S R L E W K K L G R S V S F V Y Y Q Q T L Q G D F K N R A E M I D F  
JAM 42 N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S

A33 101 S I T I D Q L T M A D N G T Y E C S V S L . M . . . . . S D L E G N T K S R V R L L V L V P P S K  
40628 93 G I T F K S V T R E D T G T Y T C M V S E . . . . . E G G N S Y G E V K V K L I V L V P P S K  
45416 97 S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V S K P T V T  
35638 93 N I R I K N V T R S D A G K Y R C E V S A P S . . . . . E Q G Q N L E E D T V T L E V L V A P A V  
JAM 92 G I T F S S V T R K D N G E Y T C M V S E . . . . . E G G Q N Y G E V S I H L T V L V P P S K

A33 144 P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q . . . . .  
40628 135 P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N . P K S T R A F  
45416 147 T G S G Y G F T V P Q G M R I S L Q C Q A R . G S P P I S Y I W Y K Q Q T N N Q E P . . . . .  
35638 137 P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S  
JAM 134 P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F

FIG.-1A

SEQ ID NO: 6 A33 186 . . . P L A Q P A S G Q P V S L K N I S T D T S G Y Y I C T S S N E E G . . . . . T Q F C N I T V  
 SEQ ID NO: 1 40628 184 S N S S Y V L N P T T G E L V F D P L S A S D T G E Y S C E A R N G Y G . . . . . T P M T S N A V  
 SEQ ID NO: 2 45416 188 . . . . . I K V A T L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D  
 SEQ ID NO: 9 35638 186 T N S S Y T M N T K T G T L Q F N T V S K L D T G E Y S C E A R N S V G . . . . . Y R R C P G K R  
 SEQ ID NO: 10 JAM 184 M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G . . . . . T A M R S E A A

A33 227 A V R S P S M N V A L Y V G I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A . .  
 40628 228 R M E A V E R N V G V I V A A Y L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S . . .  
 45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A G P G K S L  
 35638 230 . M Q V D D L N I S G I I A A V V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S . .  
 JAM 228 H M D A V E L N V G G I V A A V L V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P . .

A33 275 . R P N R E A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
 40628 275 . . . . . S K K V I Y S Q P S A R S E G E F K Q T S S F L V . . . . .  
 45416 283 P V F A I I L I I S L C C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R . . . . .  
 35638 277 . N S S S K A T T M . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F . . . . .  
 JAM 276 . . . . . G K K V I Y S Q P S T R S E G E F K Q T S S F L V . . . . .

FIG. 1B

## SEQ ID NO:1

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr  
 1 5 10 15 20 25 30  
 Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val  
 35 40 45 50 55 60  
 Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu  
 65 70 75 80 85 90  
 Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr Gly  
 95 100 105 110 115 120  
 Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val  
 125 130 135 140 145 150  
 Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr  
 155 160 165 170 175 180  
 Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr  
 185 190 195 200 205 210  
 Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 215 220 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys  
 245 250 255 260 265 270  
 Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 275 280 285 290 295 299

FIG.\_2

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SEQ ID NO:2

1 MGILLGLLLL GHLTVDTYGR PILEVPESVT GPWKGDNLP CTYDPLQCYT QVLVKNLVQR GSDPTIFLR DSSGDHIQQA KYQRLHVSH KVPGDVSLQL

101 STLEMDRRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTCGS YGFTVPQCMR ISLQCCARGS PPISYIWKQ QTNQEPKV ATLSLLFKP  
^Glycosaminoglycan attachment site

201 AVIADSGSYF CTAKQVGSE QHSDIVKFW KDSSKLLKTK TEAPTMTYP LKATSTVKQS WDWTDMGY LGETSAGPGK SLPVFAILLI ISLCCMVVFT  
^Transmembrane domain

301 MAYIMLCRKT SQEHVYEA R

# FIG.\_3

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OLI2162 (35936.f1)  
SEQ ID NO:12

TCGCGAGCTGTGTTCTGTTTCCC

OLI2166 (35936.f3)  
SEQ ID NO:16

TTGCCTTACTCAGGTGCTAC

OLI2163 (35936.p1)  
SEQ ID NO:13

TGATCGCGATGGGACAAAGCGCAAGCTCGAGAGGAACTGTTGTGCCT

OLI2167 (35936.r2)  
SEQ ID NO:17

ACTCAGCAGTGGTAGGAAAG

OLI2164 (35936.f2)  
SEQ ID NO:14

ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)  
SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

# FIG.\_8

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DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50  
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100  
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150  
CATCCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200  
AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250  
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300  
TGTCTTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350  
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

**FIG.\_4A**

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50  
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100  
GCGCAAGCTC GAGAGGAAAC TGTGTGCCT CTTCATATTG GCGATCCTGT 150  
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200  
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGT GCCTACTCGG 250  
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300  
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350  
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400  
CTGGGACATA CACTTGATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450  
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500  
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550  
CAGAACAAGA TGGTTCCCCA CTTTCTGAAT ACACCTGGTT CAAAGATGGG 600  
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650  
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700  
CCTCTGATAC TGGAGAATAC AGCTGT 726

**FIG.\_4B**

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50  
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100  
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150  
TAAGATTACT GAGCTCCGTG TCCAGAACT CTCTGTCTCC AAGCCCACAG 200  
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250  
AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300  
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350  
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400  
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450  
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500  
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550  
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600  
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTG TG 650  
CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700  
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750  
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800  
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850  
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900  
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950  
AGGGCAAAAG TGTCTGTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000  
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050  
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100  
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150  
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200  
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250  
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300  
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350  
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400  
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450  
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500  
AAA 1503

**FIG. 4C**

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SEQ ID NO:11 GGAGTCCTT CGCGGGCTGT TGTGTCAGTG GCCTGATCGC GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100  
TGGCGATCCT GTTGTGCTCC CTGGCATTGG GCAGTGTTAC AGTGCACCTT TCTGAACCTG AAGTCAGAAAT TCCTGAGAAT AATCCTGTGA AGTTGTCTCTG 200  
TGCCTACTCG GGCTTTTCTT CTCCCGGTGT GGAGTGAAG TTGAGCCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300  
GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCITCA AGTCCGTGAC ACGGAAGAC ACTGGGACAT ACACTGTAT GGTCTCTGAG GAAGGCGCA 400  
ACAGCTATGG GGAGGTCAAG GTCAGACTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCCTCTGCC ACCATTGGGA ACCGGGCAGT 500  
GCTGACATGC TCAGAACAAG ATGTTTCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAAGCAC CCGTGGCTTC 600  
AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700  
GGTATGGGAC ACCCATGACT TCAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800  
GGGAATCTTG GTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCACCTTGG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900  
AGTCCCGGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCGTGTTG AGCTGGTGG GCTCACCGCC TATCATCTGC ATTTGCCCTA CTCAGGTGCT 1000  
ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC CCTTACTTCT TCGGATGTGT TTTTAAATAAT 1100  
GTCAGCTATG TGCCCCATCC TCCCTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAAT TGTTTAAAGT GTTTTATCCC CATTTCTTTG 1200  
AGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGT GGCAGGAATC TGCACCTCAAC TGCCACCTG 1300  
GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT TGGGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400  
CTAGAGCGGC TGAATGGTT GTTGGTGAT GACACTGGGG TCTTCCATC TCTGGGCC ACTCTCTTCT GTCTTCCC ACTGGAGTCCC ACTGGATCC 1500  
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGTGCTGT GGAAATGGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600  
TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCAG CCTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700  
TCACCTGAGG TCGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAT ACAAGTTAG CCAGGCATGG TGGTGCATGC CTGTAGTCCC 1800  
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG. 5



SEQ ID NO:7

1 CCCACCGCTC CGCCACGCG TCCGCCCCACG GGTCCGCCCA CCGCTCCGGG CCACCAGAG TTTGAGCCTC TTTGGTAGCA GGAGGCTGGA AGAAGGACA  
GGGTGCGCAG CGCGTGCGC AGCGGGGTGC CCAGGGGGGT GCGCAGGCCC GGTGCTCTTC AACTCGGAG AAACCATCGT CCTCCGACCT TCTTTCCTGT

101 GAAGTAGCTC TGGGTGTGAT GGGGATCTTA CTGGGCTGTC TACTCTCTGG TACTCTCTGG GCACCTAACA GTGCACACTT ATGCCGCTCC CATCTGGAA GTGCCAGAGA  
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGAGC ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT

1 SEQ ID NO:2 M G I L L G L L L L G H L T V D T Y G R P I L E V P E S  
^MET

201 GTGTAACAGG ACCTTGAAA GGGGATGTGA ATCTTCCCTG CACCTATGAC CCCCTGCAAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG  
CACATTGTCC TGGAACTTTT CCCCTACACT TAGAAGGAC GTGGTACTG GGGGACCTTC CGATGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC

29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCT GTACCATCT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACAGGGC CGCTGTCATG TGAGCCACAA GGTTCACAGA  
GAGCTGGGA CAGTGGTAGA AAGATGCACT GAGAAGACCT CTGCTATAGG TCCTCCGTTT CATGCTCCCG GCGACGTAC ACTCGGTGTT CCAAGGTCTT

62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACGTGTGAA GTACCTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG  
CTACATAGG AGGTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTGTGTT CAGCACTCTC

95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAGATTAC TGAGTCCGT GTCCAGAAAC TCTCTGTCTC CAAGCCACA GTGACAACTG GCACGGTTA TGGCTTCACG GTGCCCCAGG GAATGAGGAT  
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAGTC CACGGGTCC CTTACTCCTA

129 K I T E L R V Q K L S V S K P T V T T G S G Y G F T V P Q G M R I

601 TAGCCTTCAA TGCAGGCTC GGGGTTCTCC TCCCATCACT TATATTGTT ATAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCCTAAGT  
ATCGGAAGTT ACGGTCCGAG CCCCAGAGG AGGGTAGTCA ATATAAACCA TATTGTTGT CTGATTATTG GTCCTTGGT AGTTTCATCG TTGGGATTCA

162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG.\_6A

SEQ ID NO:7 701 ACCTTACTCT TCAAGCCCTGC GGTGATAGCC GACTCAGGCT CCTATTCTTG CACTGCCAAG GCCCAGGTTG GCTCTGACCA GCACAGCCAC ATTCTGAAGT  
TGAATGAGA AGTTCCGACG CCACTATCGG CTAGTCCGA GGATAAGAC GTGACGGTTC CCGTCCAC CGAGACTCGT CGTGTGCTG TAACACTTCA  
SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCCCT GAAAGCAACA TCTACAGTGA AGCAGTCCTG  
AACACCAGTT TCTGAGGAGT TTGCGATGAGT TCTGTTCTG ACTCCGTGGA TGTGGTACT GTATGGGGA CTTTCGTTGT AGATGCTCACT TCGTCAGGAC  
229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGA CTGGACC ACTGACATGG ATGGCTACCT TGGACAGACC AGTCTGGG CAGGAAAGAG CTTGCCCTGC TTGCCATCA TCCTCATCAT CTCCTTGTGC  
CTGACCTGG TGA CTGTACC TACCGATGGA ACCTCTCTGG TCAGGACCCG GTCCTTTCTC GGACGGACAG AACGGTAGT AGGAGTAGTA GAGGACACG  
262 D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGATGTGG TTTTACCAT GGCCTATATC ATGCTCTGTC GGAACATC CCAACAGAG CATGTCTAGC AAGCAGCCAG GTAAGAAAGT CTCCTCTCTT  
ACATACCACC AAAAATGTA CCGGATATAG TACAGACAG CTTTCTGTAG GGTGTTCTC GTACAGATGC TTGTCGCTC CATTCTTTCA GAGAGGAGAA  
295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCCTCCT GGCCTCAATT TTGATTACTG GCAGGAATG TGGAGGAAG GGGGTGTGC ACAGACCCAA TCCTAAGGCC GGAGGCCTTC  
GGTAAAACT GGGGCAGGA CGGAGCTTAA AACTAATGAC CGTCTTTAC ACCTCCTTCC CCCCACACCG TGTCTGGGT AGGATTCCGG CCTCCGGAAG

1201 AGGTCAGGA CATAGTCCC TTCCCTCTCT CAGGCACCTT CTGAGGTTGT TTGGCCCTC TGAACACAAA GGATAATTTA GATCCATCTG CCTTCTGCTT  
TCCCAGTCTT GTATCGACGG AAGGAGAGA GTCCGTGGA GACTCCAACA AAACCGGGAG ACTTGTGTTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAATCC TGGTGTGTAG GATCTGATA ATTAATTGGC AAGAAATGAG GCAGMAGGT GGGAAACCAG GACCACAGCC CCAAGTCCCT TCTTATGGGT  
GGTCTTAGG ACCCACCATC CTAGGACTAT TAATTAACCG TTCTTAAC TCCTTCCCA CCCTTTGGTC CTGGTGTGG GTTCAGGGA AGAATACCCA

1401 GGTGGGCTT TGGGCCATAG GGCACATGCC AGAGAGGCCA ACCACTCTGG AGAACCATG AGGGTGCCA TCTTCGCAAG TGGCTGCTCC AGTATGAGC  
CCACCCGAGA ACCCGGTATC CCGTGTACCG TCTCTCCGT TCGTGAGACC TCTTTGGTAC TCCCACCCGT AGAAGCGTTC ACCGAGGAGG TCACACTCTG

1501 CAACCTCCCA GAATCTGGC AACAACTACT CTGATGAGCC CTGCATAGGA CAGGAGTACC AGATCATGCC CCAGATCAAT GGCAACTAGC CCCCCTCTGT  
GTGAAGGCT CTAGACCCG TTGTTGATGA GACTACTCGG GAGGTATCCT GTCCTCATGG TCTAGTAGCG GGTCTAGTTA CCGTTGATGC GGGCGGACGA

FIG. 6B

SEQ ID NO:7

1601 GGACACAGTT CCTCTGGATT ATGAGTTTCT GGCACCTGAG GGCAAAAGTG TCTGTTAAAA ATGCCCCATT AGCCAGGAT CTGCTGACAT AATTGCCTAG  
CCTGTGTCAA GGAGACCTAA TACTCAAAGA CCGGTGACTC CCGTTTTCAC AGACAAATTTT TACGGGGTAA TCCGGTCTTA GACGACTGTA TTAACGGATC

1701 TCAGTCCCTG CCTTCTGCAT GGCCTTCTTC CCTGCTACCT CTCTTCCTGG ATAGCCCAA GTCTCCGCTT ACCAACACTG GAGCCGCTGG GAGTCACTGG  
AGTCAGGAAC GGAAGACGTA CCGGAAGAAG GGACGATGGA GAGAAGGACC TATCGGGTTT CACAGGCCGA TGGTTGTGAC CTCGGCGACC CTCAGTGACC

1801 CTTTGCCCTG GAATTGGCA GATGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCTTCTAG TATCTCTGCC GGGGGCTTCT GGTACTCCTC  
GAAACGGGAC CTTAAACGGT CTACGTAGAG TTCAATTCGGT CGACGACCTA AACCAGACC CCGGAAGATC ATAGAGACGG CCCCCGAAGA CCATCAGGAG

1901 TCTAAATACC AGAGGGAAGA TGCCCATAGC ACTAGGACTT GGTCAATCATG CCTACAGACA CTATTCMACT TTGGCATCTT GCCACCAGAA GACCCGAGGG  
AGATTTATGG TCTCCCTTCT ACGGTATCG TGATCCTGAA CCAGTAGTAC GGATCTCTGT GATAAGTTGA AACCGTAGAA CCGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CTGCCAGCTC AGAGGACCAG CTATATCCAG GATCATTTCT CTTTCTTCAG GCCCAGACAG CTTTAAATG AAATGTTAT TTCACAGGCC  
TCCGAGTCA GACGGTCGAG TCTCCTGGTC GATATAGCTC CTAGTAAAGA GAAAGNAGTC CCGTCTGTG CAAATTAAC TTAAACAATA AAGTGTCCGG

2101 AGGGTTCAGT TCTGCTCCTC CACTATAAGT CTATGTTCT GACTCTCTCC TGGTGCTCAA TAAATATCTA ATCATAACAG C  
TCCCAAGTCA AGACGAGGAG GTGATATTCA GATTACAGA CTCAGAGAGG ACCACAGTT ATTTATAGAT TAGTATTGTC G

FIG.\_6C

CCGAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCT  
CAGAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT  
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC  
CCCAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA  
AACCCCAAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTTCGGAGTGTCTC  
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA  
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT  
TAGTGCCCCATCTGAGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT  
AGTGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGT  
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTTAAGGA  
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAAC  
AATGAATACAAAACCTGGAAGTCTGCAATTTAATACTGTTTCCAACTGGAGACTGGAGA  
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA  
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT  
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC  
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG  
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA  
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAATTAG  
CTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGCTTGGGAGACAGGAGAATCACTTGA  
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA  
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATAAATAAATAA  
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

**FIG. 7**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR  
LEWKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN  
LEEDTVTLEVLVAPAVPSCCEVPSSALS GTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR  
LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGI  
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW  
KAAAGGSRGOEF

**FIG. 11**

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SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GAGGCACMAG GTTCCAGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC  
 CGTCCGTTTC ATGGTCCCG CGGACGTACA CTCGGTGTTT CNAAGTCTTC TACATAGGA GGTAACTCG TGGGACCTCT ACCTACTGGC CTCGGTGATG  
 ^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCMAACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCACAG  
 TCCACACTTC AGTGGACCGT CTGAGGACTA CCGTTGGTTC AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCGGGTGTC

201 TCACAACCTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATCAGGATT AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTGCT  
 ACTGTTGACC GTCGCCCAATA CCGAAGTGCC ACGGGGTCCC TTAAGTCTTA TCGGAAGTTA CCGTCCCAAG CCCCAGAGG AGGTAGTCA ATATAAACCA

301 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCTAAG TACCTTACTC TTCMAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT  
 TATTGTTGT CTGATTATTG GTCCCTTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTCCGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCAGTGCCAA GGGCCAGGTT GGCTCTGACC AGCAGACCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAGACTACTC AAGACCAAGA CTGAGGCACC  
 CCGTACGGTT CCCGGTCCAA CCGAGACTCG TCGTGTGGCT GTAACACTTC AAACACCAGT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTGG  
 ^42257.r1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAGCCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTCTGGG  
 ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTCGTACCGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCAGGACCC

601 CCAGGAAAGA GCCTGCCTGT CTTGGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT  
 GGTCTTTCT CCGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAC CAAAATGGT ACCGGATATA GTACGAGACA GCCTTCTGTA  
 ^42257.f2 SEQ ID NO:19

701 CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC AAGCACTCTG GAGAAACCAT GAGGGTGGC ATCTTCGCA GTGGCTGCTC  
 GGGTGTCTT CGTACAGATG CTTGCTGGT CCCGTGTAG GTCTCTCCGG TTGCTGAGAC CTCTTTGGTA CTCCCACCG TAGAAGCGT CACCGAGGAG

FIG.\_9A

SEQ ID NO:5

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCACAACTA CTCTGATGAG CCCTGCATAG GACAGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA  
GTCACACTC GGTGAAGG TCTTAGACCC CCGTGTGAT GAGACTACTC GGGACGATC CTGTCTCAT GGTCTAGTAG CCGGTCTAGT TACCGTTGAT

901 CGCCCGCGTG CTGGACACAG TTCTCTGGA TTATGAGTT CTGGCCACTG AGGCALAAAG TGTCTGTTAA AATGCCCCA TTAGGCCAGG ATCTGCTGAC  
GCGGCGGAC GACCTGTGTC AAGGAGACCT AATACTCAA GACCGGTGAC TCCCGTTTC ACAGACAATT TTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAATTGCT AGTCACTCT TGCCTTCTGC ATGGCTTCT TCCCTGCTAC CTCTCTTCTT GATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT  
TATTAACGGA TCAGTCAGGA ACGAAGACG TACCGGAAGA AGGACGATG GAGAGAAGGA CCTATCGGT TTCACAGGCG GATGTTGTG ACCTCGGCGA

1101 GGGAGTCACT GGCCTTCCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT  
CCCTCAGTGA CCGAAACGGG ACCTTAACG GTCTACGTAG AGTTCATTCTGTCGACGACC TAAACCGAGA CCGGGGAAGA TCATAGAGAC GGGCCCCGAA  
^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAATA CCAGAGGGAA GATGCCCAT GATGGTATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG  
GACCATGAGG AGAGATTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCAGTAGT ACGGATCTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCAAT TCTCTTCTT CAGGGCCAGA CAGCTTTTAA TTGAATTTGT  
TTCTGGGCTC CCCTCCAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTAGTAA AGAGAAGAA GTCCCGGTCT GTCGAAATTT AACTTTAACA

1401 TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCTACTATA AGTCTAATGT TCTGACTCTC TCCTGGTGT CAATAAATAT CTAATCATAA CAGCAAAAA  
ATAAGTCTC CCGTCCCAAG TCAAGACGAG GAGCTGATAT TCAGATTACA AGACTGAGAG AGGACCAGGA GTTATTATA GATTAGTATT GTCGTTTTTT

1501 AAA

TTT

FIG.-9B

A33\_HUMAN A33 ANTIGEN PRECURSOR - HOMO SAPIENS FRAME SCORE MATCH PCT  
+1 246 81 30

A33\_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR--VEW-KFDQGDTRRLVC--YNN  
SEQ ID NO:23

A33\_human 17 VTVDAISVETPQDVLRLASQKSVTLPTCYHTSTSSREGLIQWDKLLLTHTERVVIWPFNS  
SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTFL-----PTGITFKSVTREDTGTYTCMVS---EEGNSYGEVKVK  
\* \* \* \* \*

A33\_human 77 KNYIHGELYKNRVVISISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR  
\* \* \* \* \*

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGPSPSEYTWFKDGIWPTNPKSTRAFSN  
\* \* \* \* \*

A33\_human 135 LLVLVPPSKPEGIEGETIIGNNIQLTCQSKESPTPQYSWKRYNINLQEQP-----  
\* \* \* \* \*

DNA40628 607 SSVVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA  
\* \* \* \* \*

A33\_human 187 ---LAQPASGQPVSCLKNISTDTSGYIYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIIV  
\* \* \* \* \*

DNA40628 775 AVLVTLLILLGILVFIWFAYSRGHFDR--KKGTSSKKVIYSQP  
\* \* \* \* \*

A33\_human 244 GVVAALLIIIGIIY---CCCCRGKDDNTEDKEDARPNREAYEEP  
\* \* \* \* \*

FIG.-10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19  
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA40628 112 LCSL--ALGSVTVHSSEPEVRIPENNPVKLSAYSGFSSPR---VEM-KFDQGDTTTRLVC  
SEQ ID NO:25

A33 human 12 LCAVRVTVD AISVETPQDVLRLASQKSVTLPCITYHTSTSSREGLIQWDKLLLTHTERVVI  
SEQ ID NO:26

DNA40628 274 --YNNK--ITAS-YEDRVTFI-----PTGITFKSVTREDTGTTCMVSEEGNSYGEVK  
A33\_human 72 WPFSENKVIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628 421 --VKLIIVLPSPKPTVNIPISSATIGNRAVLTCEQDQSPPEYTWFKDGIVMPTNPKSTR  
A33\_human 131 SRVRLIVLPSPKPEGIEGETIIGNNIQLTCQSKESPTPOYSWKRYNINLQEQP----

DNA40628 595 AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV--  
A33\_human 187 -----LAQPASGQPVSLKNISTDTSGYICTSSNEEGTQFCNITVAVRSPSMNVALYV

DNA40628 766 -IVAAVLVTLLILGILVFIWFAYSRGHFDRT--KKGTSKKVIYSQP  
A33\_human 240 GIAVGVAALIIIGIIY---CCCCRGKDDNTEDKEDARPNREAYEEP

FIG.\_10B



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**FIG. 12**

SEQ ID NO: 6	A33_hum	1	M	V	G	K	M	W	P	V	L	W	T	L	C	A	V	R	V	T	V	D	A	I	S	V	E	T	P	Q	D	V	L	R	A	S	Q	G	K	S	V	T	L	P	C	T	Y	H	T	S	T	S
SEQ ID NO: 2	45416	1	M	G	I	L	L	G	L	L	L	G	H	L	T	V	D	T	Y	G	R	P	I	L	E	V	P	E	S	V	T	G	P	W	K	G	D	V	N	L	P	C	T	Y	D	P	L	Q	G			
A33_hum	51	S	R	E	G	L	I	Q	W	K	L	L	L	T	H	T	E	R	V	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N	A	E	Q	S	D				
45416	49	Y	T	Q	V	L	V	K	W	L	V	Q	R	G	S	D	P	V	T	I	F	L	R	D	S	S	G	D	H	I	Q	Q	A	K	Y	Q	G	R	L	H	V	S	H	K	V	P	G	D				
A33_hum	100	A	S	I	T	I	D	Q	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	M	S	D	L	E	G	N	T	K	S	R	V	R	L	L	V	L	V	P	P	S								
45416	96	V	S	L	Q	L	S	T	L	E	M	D	O	R	S	H	Y	T	C	E	V	T	W	Q	T	P	D	G	N	Q	V	V	R	D	K	I	T	E	L	R	V	Q	K	L	S	V	S	K	P	T	V	
A33_hum	143	K	P	E	C	G	I	E	G	E	T	I	I	G	N	N	I	Q	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	O	P	A	S	
45416	146	T	T	G	S	G	Y	G	F	T	V	P	Q	G	M	R	I	S	L	Q	C	O	A	R	G	S	P	I	S	Y	I	W	Y	K	Q	O	T	N	N	Q	E	P	I	K	V	A	T					
A33_hum	193	G	O	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	Q	F	C	N	I	T	V	A	V	R	S	P	S	M	N	V	A	L	Y	V	G				
45416	193	L	S	T	L	L	F	K	P	A	V	I	A	D	S	G	S	Y	F	C	T	A	K	G	Q	V	G	S	E	O	H	S	D	I	V	K	F	V	K	D	S	S	K	L	L	K	T	X	T	E		
A33_hum	241	I	A	V	G	V	V	A	A	L	I	I	G	I	I	Y	C	C	C	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	P	E	Q	L	R	E			
45416	243	A	P	T	T	M	T	Y	P	L	K	A	T	S	T	V	K	S	W	D	W	T	T	D	M	D	G	Y	L	G	E	T	S	A	G	P	G	K	S	L	P	V	F	A	I	L	I	S				
A33_hum	291	L	S	R	E	R	E	E	E	D	D	Y	R	O	E	E	O	R	S	T	G	R	E	S	P	O	H	L	D	O																						
45416	293	L	C	C	H	V	V	F	T	M	A	Y	I	H	L	C	R	K	T	S	Q	Q	E	H	V	Y	E	A	A	R																						

FIG.-13

SEQ ID NO: 6	A33_hum	1	..	M	V	G	K	M	P	V	L	W	T	L	C	A	V	R	V	T	V	D	..	..	A	I	S	V	E	T	P	O	D	V	L	R	A	S	Q	G	K	S	V	T	L	P	C					
SEQ ID NO: 9	35638	1	M	A	R	R	S	R	H	R	L	L	L	L	L	R	Y	L	V	V	A	L	G	Y	H	K	A	Y	G	F	S	A	P	K	D	O	Q	V	V	T	A	V	E	Y	O	E	A	I	L	A	C	
A33_hum		44	T	Y	H	T	S	T	S	S	R	E	G	L	I	Q	W	K	L	L	T	H	T	E	R	V	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N		
35638		51	..	K	T	P	K	T	V	S	S	R	L	E	W	K	L	..	..	..	..	..	..	..	G	R	S	V	S	F	V	Y	Y	Q	T	..	L	Q	G	D	..	F	K	N	R	..	..	..				
A33_hum		94	N	A	E	Q	S	D	A	S	I	T	I	D	O	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	M	S	D	L	E	G	N	..	T	K	S	R	V	R	L	L	V	L	V	P	P	S
35638		87	..	A	E	M	I	D	F	N	I	R	I	K	N	V	T	R	S	D	A	G	K	Y	R	C	E	V	S	A	P	S	E	O	G	O	N	L	E	E	D	T	V	T	L	E	V	L	V	A	P	A
A33_hum		143	K	P	E	C	G	I	E	G	E	T	I	I	G	N	I	Q	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	Q	P	A	S	
35638		136	V	P	S	C	E	V	P	S	S	A	L	S	G	T	V	V	E	L	R	C	Q	D	K	E	G	N	P	A	P	E	Y	T	W	F	K	D	G	I	R	L	L	E	N	P	R	L	G	S	Q	S
A33_hum		193	G	O	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	O	F	C	N	I	T	V	A	V	..	..	R	S	P	S	M	N	V	A	L	Y	V		
35638		186	T	N	S	S	Y	T	M	N	T	K	T	G	T	L	Q	F	N	T	..	V	S	K	L	D	T	G	E	Y	S	C	E	A	R	N	S	V	G	Y	R	R	C	P	G	K	R	M	Q	V	D	D
A33_hum		240	G	I	A	V	G	V	V	A	A	L	I	I	G	I	I	Y	C	C	..	..	C	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E	A	Y	E	E	P	P	E			
35638		235	L	N	I	S	G	I	I	A	V	V	V	V	A	L	V	I	S	V	C	G	L	G	V	C	Y	A	Q	R	K	G	Y	F	S	K	E	T	S	F	Q	K	S	N	S	S	S	K	A	T	T	
A33_hum		287	Q	L	R	E	L	S	R	..	E	R	E	E	E	D	D	Y	R	Q	E	E	Q	R	S	T	G	R	E	S	P	O	H	L	O	Q																
35638		285	M	S	E	N	V	O	W	L	T	P	V	I	P	A	L	W	K	A	A	A	G	G	S	R	G	Q	E	F																						

FIG.-14

SEQ ID NO: 10	jam	1	M	G	T	E	G	K	A	G	R	K	L	L	F	L	F	T	-	S	M	I	L	G	S	L	V	Q	G	K	G	S	V	Y	T	A	Q	S	D	V	Q	V	P	E	N	E	S	I	K	L	T	C
SEQ ID NO: 1	40628	1	M	G	T	K	A	Q	V	E	R	K	L	L	C	L	F	I	L	A	I	L	L	C	S	L	A	L	G	S	V	T	V	H	S	S	E	P	E	V	R	I	P	E	N	N	P	V	K	L	S	C
jam		50	T	Y	S	G	F	S	S	P	R	V	E	W	K	F	V	Q	G	S	T	T	A	L	V	C	Y	N	S	Q	I	T	A	P	Y	A	D	R	V	T	F	S	S	G	I	T	F	S	S	V	T	
40628		51	A	Y	S	G	F	S	S	P	R	V	E	W	K	F	D	Q	G	D	T	T	R	L	V	C	Y	N	N	K	I	T	A	S	Y	E	D	R	V	T	F	L	P	T	G	I	T	F	K	S	V	T
jam		100	R	K	D	N	G	E	Y	T	C	M	V	S	E	E	G	G	Q	N	Y	G	E	V	S	I	H	L	T	V	L	V	P	P	S	K	P	T	I	S	V	P	S	S	V	T	I	G	N	R	A	V
40628		101	R	E	D	T	G	T	Y	T	C	M	V	S	E	E	G	G	N	S	Y	G	E	V	K	V	K	L	I	V	L	V	P	P	S	K	P	T	V	N	I	P	S	S	A	T	I	G	N	R	A	V
jam		150	L	T	C	S	E	H	D	G	S	P	P	S	E	Y	S	W	F	K	D	G	I	S	M	L	T	A	D	A	K	K	T	R	A	F	M	N	S	S	F	T	I	D	P	K	S	G	D	L	I	F
40628		151	L	T	C	S	E	Q	D	G	S	P	P	S	E	Y	T	W	F	K	D	G	I	-	V	M	P	T	N	P	K	S	T	R	A	F	S	N	S	S	Y	V	L	N	P	T	T	G	E	L	V	F
jam		200	D	P	V	T	A	F	D	S	G	E	Y	Y	C	Q	A	Q	N	G	Y	G	T	A	W	R	S	E	A	A	H	M	D	A	V	E	L	N	V	G	G	I	V	A	A	V	L	V	T	L	I	L
40628		200	D	P	L	S	A	S	D	T	G	E	Y	S	C	E	A	R	N	G	Y	G	T	P	M	T	S	N	A	V	R	M	E	A	V	E	R	N	V	G	V	I	V	A	A	V	L	V	T	L	I	L
jam		250	L	G	L	L	I	F	G	V	W	F	A	Y	S	R	G	Y	F	E	T	K	K	G	T	A	P	G	K	K	V	I	Y	S	O	P	S	T	R	S	E	G	E	F	K	Q	T	S	S	F	L	
40628		250	L	G	I	L	V	F	G	I	W	F	A	Y	S	R	G	H	F	D	R	T	K	K	G	T	-	S	S	K	K	V	I	Y	S	O	P	S	A	R	S	E	G	E	F	K	Q	T	S	S	F	L
jam		300	V																																																	
40628		299	V																																																	

FIG.\_15

20/24

SEQ ID NO: 10 jam 1 MGTEGKAGRKLLFLFTSMILGSLVOGKG.SVYTAQSDVQVPPENESIKLT  
SEQ ID NO: 2 45416 1 .....MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPT

jam 49 CTYS...GFSSPRVEWKFFVQGSTTALV...CYNQA.TAPYADRVTFS.  
45416 41 CTYDPLQGYTQVLVKWLVRGSDPVTIFLRDSSGDHIIQQAKEYQGRHLHVS.H

jam 90 ....SSGITFSSVTRKDNGEYTCMV...SEEGQNYGEVSIHLTVL.VPP  
45416 91 KVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSV

jam 132 SKPTISVPS....SVTIGNRAVLTCSSEHDGSPPSSEYSWFKDGISMLTADA  
45416 141 SKPTVTTGSGYGFTVPQGMRLISLQCQAR.GSPPISYIWKQQTN...NQEP

jam 178 KKTRAFNMNSSFTIDPKSGDLIFDPVTAFDSGEYCYCQAQNGYGTAMRSEAA  
45416 188 IKVATL.....STLLFKPAVIA.DSGSYFCTAKGOVGSEQHSDIV

jam 228 H...MDAVELNVGGIVAAVLVTLILLGLLIFG...VWFAYSRYGFETTKK  
45416 227 K FVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTOMDGYLGETSA

jam 272 GTAPGKKVIYSQPSTRSEGEFKQTS SFLV  
45416 277 GPGKSLPVFAIILISLCCMVVFTMAYIMLCRKTSQQEHVYEAA.R

FIG.\_16

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V O G K G S V Y T A Q S D V Q V . . . P E N E S I K L  
SEQ ID NO: 29 35638 1 . . . M A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K Q Q V V T A V E Y Q E A I L

jam 48 T C . T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S G I T F S  
35638 49 A C K T P K K T V S S R L E W K K L . G R S V S F V Y Y Q Q T L O G D F K N R A E M I D F N I R I X

jam 97 S V T R K D N G E Y T C M V S . . E E G G Q N Y G E V S I H L T V L V P P S K P T I S V P S S V T I  
35638 98 N V T R S D A G K Y R C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S

jam 145 G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S  
35638 148 G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L . E N P R L G S Q S T N S S Y T M N T K T

jam 195 G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A V E L N V G G I V A A V L  
35638 197 G T L Q F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M Q V D D L N I S G I I A A V V

jam 245 V T L I L L G L L I F G V W F A Y S R G Y F E T T X K G T A P G K K V I Y S Q P S T R S E G E F K Q  
35638 246 V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F Q K S N S S S K A T T M S E N V Q W L

jam 295 T S S F L V  
35638 293 T P V I P A L W K A A A G G S R G Q E F

FIG. 17

SEQ ID NO: 6	A33_hum	1	...	MV	GK	MWPV	L	WT	·	L	CA	VR	VT	VD	A	I	SV	ET	P	Q	DV	LR	AS	QG	KS	SV	TL	P	CT																								
SEQ ID NO: 10	jam	1	MG	TE	GK	AG	RK	LL	F	L	FT	SM	IL	GS	LV	OG	KS	SV	YT	A	Q	SD	VQ	VP	EN	ES	IK	LT	CT																								
A33_hum		45	Y	H	T	S	S	R	E	G	L	I	Q	W	K	L	L	T	H	T	E	R	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	S	N							
jam		51	Y	S	G	F	S	S	P	R	·	·	·	V	E	W	·	K	F	V	Q	G	S	T	T	A	L	V	C	·	·	Y	N	S	Q	·	·	I	T	A	P	·	Y	A	D	R	V	T	F	S	S		
A33_hum		95	A	E	Q	S	D	A	S	I	T	I	D	Q	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	M	S	D	L	E	G	N	T	K	S	R	V	R	L	L	V	L	P	P	S	K	P		
jam		91	·	·	·	·	·	·	·	S	G	I	T	F	S	S	V	T	R	K	D	N	G	E	Y	T	C	M	V	S	E	E	G	G	·	Q	N	Y	G	E	V	S	I	H	L	T	V	L	P	P	S	K	P
A33_hum		145	E	C	G	I	E	G	E	T	I	I	G	N	N	I	Q	L	T	C	Q	S	K	E	G	S	P	T	P	Q	Y	S	W	K	R	Y	N	I	L	N	Q	E	Q	P	L	A	Q	P	A	S	G	Q	
jam		135	T	I	S	V	P	S	S	V	T	I	G	N	R	A	V	L	T	C	S	E	H	D	G	S	P	S	E	Y	S	W	F	K	D	G	I	S	M	L	T	A	D	A	K	K	T	R	A	F	M		
A33_hum		195	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	I	C	T	S	S	N	E	E	G	T	Q	F	C	N	·	·	·	·	·	I	T	V	A	V	R	S	P	S	M	N	·	·	·	V	A	L	
jam		185	N	S	S	F	T	I	D	P	K	S	G	D	L	I	F	D	P	V	T	A	F	D	S	G	E	Y	C	Q	A	Q	N	G	Y	G	T	A	M	R	S	E	A	A	H	M	D	A	V	E	L		
A33_hum		238	Y	V	·	G	I	A	V	G	V	V	A	A	L	I	I	I	G	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I			
jam		235	N	V	G	G	I	V	A	A	V	L	V	T	L	I	L	L	G	L	L	I	F	G	V	W	F	A	Y	S	R	G	Y	F	E	·	T	T	K	K	G	T	A	P	G	K	K	V	I	Y	S		
A33_hum		284	P	P	E	Q	L	R	E	L	S	R	E	R	E	E	E	D	Y	R	Q	E	E	Q	R	S	T	G	R	E	S	P	D	H	L	D	Q																
jam		284	P	S	T	R	S	E	G	E	F	K	Q	T	S	S	F	L	V																																		

FIG.\_18

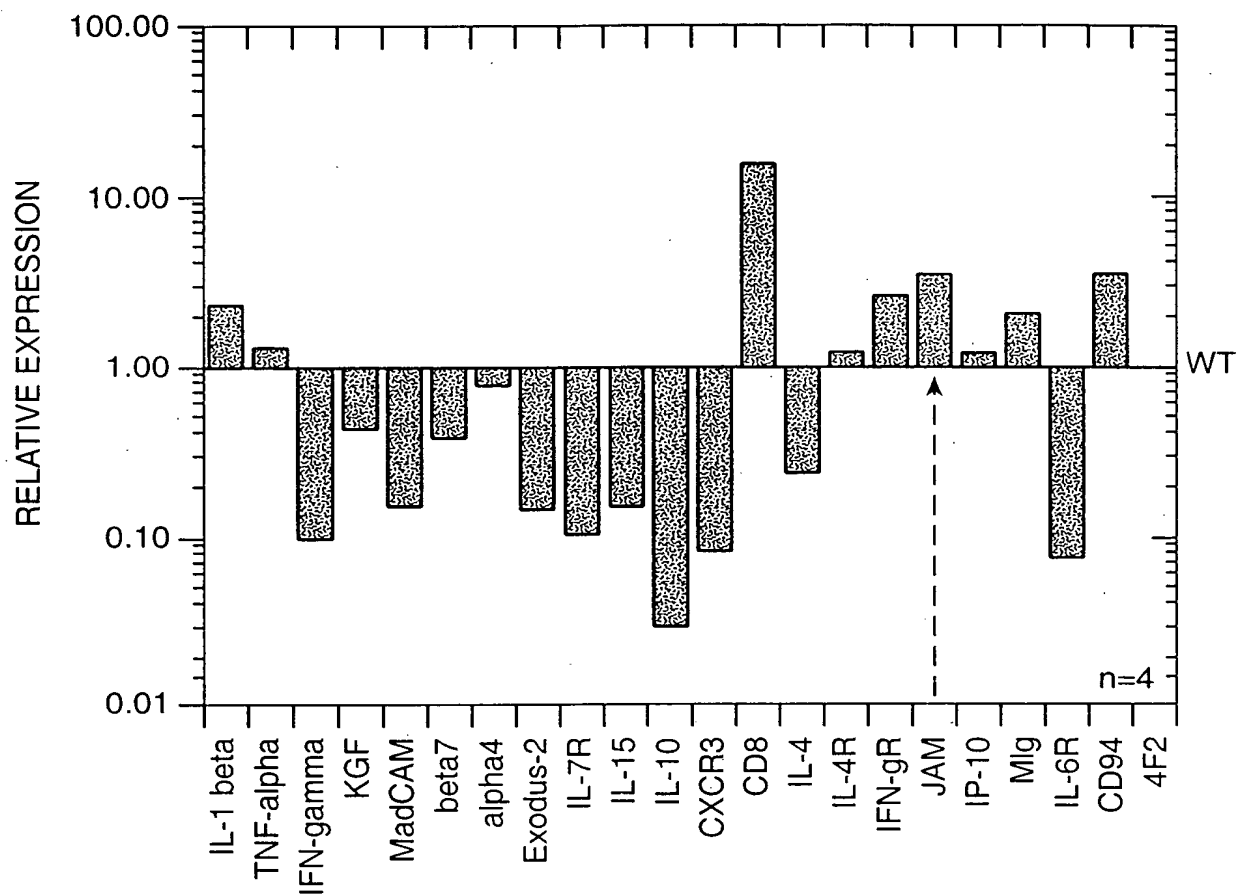
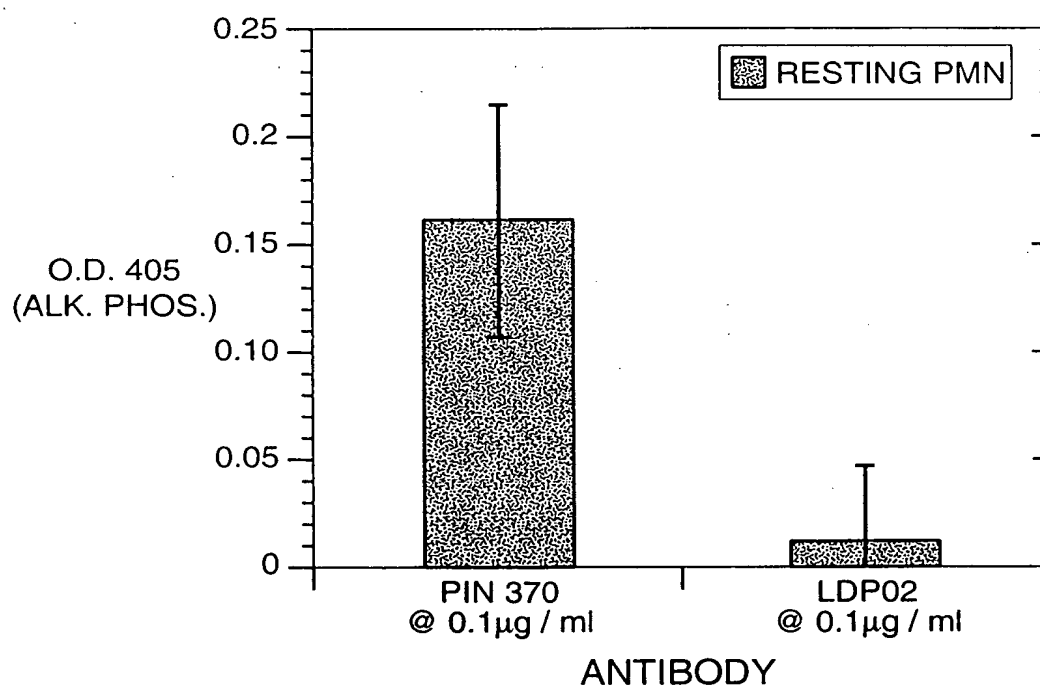
<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++		
PUTAMEN	+	OVARY	+++	APPENDIX	+
SUSTANTIA NIGRA	+	PANCREAS	++	LUNG	+++
TEMPORAL LOBE	+	PITUITARY GLAND	++	TRACHEA	+++
THALAMUS	+	ADRENAL GLAND	++	PLACENTA	+++
NUCLEUS ACCUMBENS	+	THYROID GLAND	++		
SPINAL CORD	-	SALIVARY GLAND	+++	FETAL BRAIN	+
		MAMMARY GLAND	++	FETAL HEART	+
				FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	+++

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FIG. 19



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**FIG. 20****FIG. 21**